

RESULT 1  
 US-10-665-883A-4  
 ; Sequence 4, Application US/10665883A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YUAN, Chong-Sheng  
 ; TITLE OF INVENTION: DETERMINATION OF IONS USING ION-SENSITIVE ENZYMES  
 ; FILE REFERENCE: 466992001100  
 ; CURRENT APPLICATION NUMBER: US/10/665,883A  
 ; CURRENT FILING DATE: 2003-09-19  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 392  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Chimeric protein  
 US-10-665-883A-4

Query Match 100.0%; Score 2047; DB 36; Length 392;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-192;  
 Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps  
 0;

SEQ 1

Qy	1	<u>MGGSGDDDDLAL</u> ALERELLVATQAVRKASLLTKRIQSEVISHKDSTTITKNDNSPVTTGD	60
Db	1	MGGSGDDDDLALALERELLVATQAVRKASLLTKRIQSEVISHKDSTTITKNDNSPVTTGD	60
Qy	61	YAAQTIIINAIAKSNFPDDKVVGEESSSGLSDAFVSGILNEIKANDEVYNKKNYKKDDFLFT	120
Db	61	YAAQTIIINAIAKSNFPDDKVVGEESSSGLSDAFVSGILNEIKANDEVYNKKNYKKDDFLFT	120
Qy	121	NDQFPLKSLEDVRQIIDFGNYEGGRKGRFWCLDPIDGTGFLRGEQFAVCLALIVDGVVQ	180
Db	121	NDQFPLKSLEDVRQIIDFGNYEGGRKGRFWCLDPIDGTGFLRGEQFAVCLALIVDGVVQ	180

SEQ 2

Qy	181	LGCIGCPNLVLSSYGAQDLKGHESFGYIFRAVRGLGAFYSPSSDAESWTKIHVRHLKDTK	240
Db	181	LGCIGCPNLVLSSYGAQDLKGHESFGYIFRAVRGLGAFYSPSSDAESWTKIHVRHLKDTK	240
Qy	241	DMITLEGVEKGHSSHDEQTAIKNKLNISKSLHLDSQAKYCLLALGLADVYLRLPIKLSYQ	300
Db	241	DMITLEGVEKGHSSHDEQTAIKNKLNISKSLHLDSQAKYCLLALGLADVYLRLPIKLSYQ	300
Qy	301	EKIWDHAAGNVIVHEAGGIHTDAMEDVPLDFGNGRTLATKGVIASSGPRELHDLVVSTSC	360
Db	301	EKIWDHAAGNVIVHEAGGIHTDAMEDVPLDFGNGRTLATKGVIASSGPRELHDLVVSTSC	360

SEQ 3

Qy	361	DVIQSRNA <u>KGELEGLPIP</u> NPLLRTGHHHHHHH	392
Db	361	DVIQSRNAKGELEGLPIP	392

note that current SEQ 4 has only 6 his, not 7.

NOTE it appears that SEQ ID NO:2 was previously known 100%:, however the combination of SEQ 2, 3 and 1 may be their true invention, if I can not find reason to to...????

RESULT 1  
S35318  
MET22 protein - yeast (*Saccharomyces cerevisiae*)  
N;Alternate names: HAL2 protein; protein O1180; protein YOL064c  
C;Species: *Saccharomyces cerevisiae*  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C;Accession: S35318; S66757  
R;Glaeser, H.U.; Thomas, D.; Gaxiola, R.; Montrichard, F.; Surdin-Kerjan, Y.; Serrano, R.  
EMBO J. 12, 3105-3110, 1993  
A;Title: Salt tolerance and methionine biosynthesis in *Saccharomyces cerevisiae* involve a putative phosphatase gene.  
A;Reference number: S35318; MUID:93345455; PMID:8393782  
A;Accession: S35318  
A;Molecule type: DNA  
A;Residues: 1-357  
A;Cross-references: UNIPROT:P32179; UNIPARC:UPI00001120E7; EMBL:X72847; NID:g298022; PIDN:CAA51361.1; PID:g298023  
R;Alexandraki, D.; Katsoulou, C.; Tzermia, M.  
submitted to the Protein Sequence Database, July 1996  
A;Reference number: S66756  
A;Accession: S66757  
A;Molecule type: DNA  
A;Residues: 1-357  
A;Cross-references: UNIPARC:UPI00001120E7; EMBL:Z74806; NID:g1419882; PID:g1419883; MIPS:YOL064c  
A;Experimental source: strain S288C  
C;Genetics:  
A;Gene: SGD:MET22; HAL2  
A;Cross-references: SGD:S0005425; MIPS:YOL064c  
A;Map position: 15L  
C;Keywords: transmembrane protein  
F;157-173/Domain: transmembrane #status predicted

Query Match 100.0%; Score 1838; DB 2; Length 357;  
Best Local Similarity 100.0%; Pred. No. 4.1e-140;  
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ALERELLVATQAVRKASLLTKRIQSEVISHKDSTTITKNDNSPVTTGDYAAQTIIINAIAK	60
Db	2	ALERELLVATQAVRKASLLTKRIQSEVISHKDSTTITKNDNSPVTTGDYAAQTIIINAIAK	61
Qy	61	SNFPDDKVVGEESSSGLSDAFVSGILNEIKANDEVYNKNYKKDDFLFTNDQFPLKSLEDV	120
Db	62	SNFPDDKVVGEESSSGLSDAFVSGILNEIKANDEVYNKNYKKDDFLFTNDQFPLKSLEDV	121
Qy	121	RQIIDFGNYEGGRKGRFWCLDPIDGTKGFLRGEQFAVCLALIVDGVVQLGCIGCPNLVLS	180
Db	122	RQIIDFGNYEGGRKGRFWCLDPIDGTKGFLRGEQFAVCLALIVDGVVQLGCIGCPNLVLS	181
Qy	181	SYGAQDLKGHESFGYIFRAVRGLGAFYSPSSDAESWTKIHVRHLKDTKDMITLEGVEKGH	240
Db	182	SYGAQDLKGHESFGYIFRAVRGLGAFYSPSSDAESWTKIHVRHLKDTKDMITLEGVEKGH	241

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Qy      241 SSHDEQTAIKNKLNISKSLHLDSQAKYCLLALGLADVLRRLPIKLSYQEKIWDHAAGNVI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      242 SSHDEQTAIKNKLNISKSLHLDSQAKYCLLALGLADVLRRLPIKLSYQEKIWDHAAGNVI 301

Qy      301 VHEAGGIHTDAMEDVPLDFGNGRTLATKGVIASSGPRELHDLVVSTSCDVIQSRNA 356
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      302 VHEAGGIHTDAMEDVPLDFGNGRTLATKGVIASSGPRELHDLVVSTSCDVIQSRNA 357

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## Interesting post filing application by same inventor:

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RESULT 1
US-11-881-179-1
; Sequence 1, Application US/11881179
; Publication No. US20080096230A1
; GENERAL INFORMATION
; APPLICANT: YUAN, Chong-Sheng
; APPLICANT:DATTA, Abhijit
; APPLICANT:LIU, Limin
; TITLE OF INVENTION: METHODS FOR ASSAYING PERCENTAGE OF GLYCATED HEMOGLOBIN
; FILE REFERENCE: 466992002000
; CURRENT APPLICATION NUMBER: US/11/881,179
; CURRENT FILING DATE: 2007-11-21
; PRIOR APPLICATION NUMBER: US 60/833,390
; PRIOR FILING DATE: 2006-07-25
; PRIOR APPLICATION NUMBER: US 60/858,809
; PRIOR FILING DATE: 2006-11-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fructosyl amino acid oxidase
US-11-881-179-1

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Query Match          9.9%; Score 203.5; DB 2; Length 472;
Best Local Similarity 23.0%; Pred. No. 5.3e-13;
Matches 122; Conservative 50; Mismatches 161; Indels 197; Gaps
25;

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Qy      1 MGGSGDDDDLALALERE---LLVATQAVRKASLLTKRIQSEVISHKDSTTITKNDNSPVT 57
        |||||||||: :   :|      :|      : : : | :| | ||
Db      1 MGGSGDDDDLALAVTKSSLLIVGAGTWGTSTALH-----LARRGYTNVTVLDYPYPVP 53

Qy      58 TGDYAAQTIIINAIAKSFPDDKVVGEESSSGLSDAFVSGILNEIKA-----NDEVYN 109
        :|| :   :||: | |      :||| |      || : :
Db      54 -----SAISAGNDVNKVISSGQYSNNKDEIE---VNEILAEAAFNGWKNDPLFK 99

Qy      110 KNYKKDDFLFT-----NDQFPLKSLEDVRQIIDFGNYE 142
        |   | :      :|| : | | | || : :

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Db	100	PYYHDTGLLMSACSQEGLDRLGVRVRPGEDPNLVELTRPEQFRKLAPEGVLQ-GDFPGWK	158
Qy	143	G--GRKGRFWCLDPIDGTKGFLRGEQFAVCLAL-IVDGVVQLGCIGCPNLVLSSYGAQDL	199
		: :   : :       :   :   :	
Db	159	GYFARSAGAWA----HARNALVAAAREAQRMGVKFVTGTPQ-----GRVVTLIFENNDV	208
Qy	200	KGH-ESFGYIFRAVR-----GLGAF--YSPSSDAESWTKIHVRHLKDT-----KDMIT	244
		:          : :    : :      : :	
Db	209	KGAVTGDGKIWRAERTFLCAGASAGQFLDFKNQLRPTAWTLVHIA-LKPEERALYKNIPV	267
Qy	245	LEGVEKG--HSSHDEQTAIK-----NKLNISKSLH-----	272
		: :  :   :  :	
Db	268	IFNIERGFFFEPDEERGEIKICDEHPGYTNMVQSADGTMMSSIPFEKTQIPKEAETRVRAL	327
Qy	273	-----LDSQAKYCLLALGLADV---YLRLPIKLSY	299
		:   :       :	
Db	328	LKETMPQLADRPFSFARICWCADTANREFLIDRHPQYHSLVLGCCASGRGFKYLP-----	382
Qy	300	QEKIWDHAAGNVIVHEAGGIHTDAME-----DVPLDFGNGRTLATKGVIA	344
		:   :                 : :	
Db	383	-----SIGNLIV-----DAMEGKVPQKIHელიკwnPDIAANRNWRDTLGRFG---	424
Qy	345	SSGPR---ELHDLVVSTSCDVIQSRNAKGELEGLPIPNLLRTGHHHHHHH	391
		:   :   :	
Db	425	--GPNRVMDFHVDVKEWTNVQYRDISKLKGELEGLPIPNLLRTGHHHHHHH	472